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## OM protein - protein search, using sw model

Run on: November 20, 1999, 15:32:38 ; Search time 13.1 Seconds

(without alignments)  
605.713 Million cell updates/sec

Title: us-09-126-945-2

Perfect score: 335

Sequence: 1 MGSA5POLSVSPSHLLP.....GIIRKPDISRLYQVHP1 335

Scoring table: OLIGO

Searched: 188963 seqs, 23686106 residues

Database: A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	14	4.2	155 1 R45451	Adenovirus E1A-F p
2	14	4.2	520 1 R78185	protein sequence o
3	14	4.2	462 1 W00167	E1A matrix metal
4	14	4.2	555 1 W49010	Polymavirus PEA3
5	8	2.4	452 1 R44556	Human HDM-FLI-1 ge
6	8	2.4	548 1 W07700	Human ETS2 repress
7	8	2.4	543 1 W07702	Mouse ETS2 repress
8	8	2.4	478 1 V01521	Chicken C-erg prot
9	8	2.4	451 1 V01520	Chicken C-11 prote
10	7	2.1	295 1 P01328	Immunoreactive hum
11	7	2.1	153 1 R13016	Deacetylcephalospo
12	7	2.1	444 1 R42293	Cephalosporium acr
13	7	2.1	346 1 R67430	Thermostable amino
14	7	2.1	905 1 W31186	Human p160 polypep
15	7	2.1	543 1 W36503	Human hyaluronate
16	7	2.1	578 1 W26765	Human hyaluronan s
17	7	2.1	521 1 W47237	Human lymphoid-spe
18	7	2.1	581 1 W47238	Human lymphoid-spe
19	7	2.1	339 1 W75169	Human secreted pro
20	7	2.1	89 1 W97655	Urinary tract BL21
21	7	2.1	45 1 W97657	Urinary tract BL21
22	7	2.1	30 1 V12590	Human 5' EST seque
23	6	1.8	14 1 P91133	Partial sequence o
24	6	1.8	294 1 P91468	Recombinant activa
25	6	1.8	191 1 P92071	Sequence of canine
26	6	1.8	254 1 P93673	Partial nucleotide
27	6	1.8	256 1 P93674	Sheep PrP gene for
28	6	1.8	3647 1 R05041	Filamentous haemag
29	6	1.8	1295 1 R05597	Sequence containin
30	6	1.8	421 1 R05801	Iso-penicillin N e
31	6	1.8	471 1 R05923	Immunogenic pneumo
32	6	1.8	471 1 R05924	Immunogenic pneumo
33	6	1.8	1664 1 P80264	Sequence of the JA
34	6	1.8	196 1 P82979	Part of canine SPN
35	6	1.8	165 1 R07360	Rat melanin-concen
36	6	1.8	1706 1 R08031	Adenyl cyclase fro
37	6	1.8	731 1 R08205	Heat resistant per
38	6	1.8	196 1 P70441	Sequence encoded b
39	6	1.8	927 1 P70768	Epsilon-Barr virus
40	6	1.8	5072 1 R11510	Ryanodine receptor
41	6	1.8	1445 1 R12108	N-terminal deleted
42	6	1.8	1705 1 P94365	Sequence of part o
43	6	1.8	283 1 P81096	Sequence of rhinov

44 6 1.8 1522 1 P93357  
45 6 1.8 528 1 W96151

Sequence of the ca  
Salmonella Sptp/LC

## ALIGNMENTS

RESULT 1  
ID R45451 standard; Protein; 155 AA.  
AC R45451;  
DT 11-JUL-1994 (first entry)  
DE Adenovirus E1A-F protein.  
KW Adenovirus; cancer; ets oncogene; Hela cell; enhancer core sequence;  
KW methylation.  
OS Human adenovirus.  
PN J05328975-A.  
PD 14-DEC-1993.  
PF 02-JUN-1992; JP-165453.  
PR 02-JUN-1992; JP-165453.  
PA (TAKI ) TAKARA SHUZO CO LTD.  
DR WPI: 94-021923/03.  
DR N-PSDB: 055149.  
PT Novel E1A-F gene - for production of adenovirus E1A-F and cancer  
PT research  
PS Claim 1; Page 5; 7pp; Japanese.  
CC A clone comprising the adenovirus E1A-F gene was isolated by  
CC screening a Hela cell cDNA library. The cDNA insert from the clone  
CC contains a 473bp open reading frame which codes for a protein  
CC having sequence R45451.  
SO Sequence 155 AA;

Query Match  
Best Local Similarity 4.2%; Score 14; DB 1; Length 155;  
Matches 14; Conservative 0; Pred. No. 6.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 KNRPAMNYDKLSRS 308  
DB 56 KNRPAMNYDKLSRS 69

RESULT 2  
ID R78185 standard; Protein; 520 AA.  
AC R78185;  
DT 09-FEB-1996 (first entry)  
DE Protein sequence of PEA3-beta -an ETS transcription factor.  
KW Transcription factor; probe; reverse transcription; PCR; primer;  
KW expression vector; E.coli; COS cell; ras; cancer cell multiplication;  
KW polyoma virus; transformation.  
OS Homo sapiens.  
FH key  
FT misc\_difference 84 Location/Qualifiers  
FT /note= "encoded by CTC"  
FT misc\_difference 126  
FT /note= "encoded by AAC"  
FT /note= "encoded by AAC"  
FT misc\_difference 500 /note= "encoded by ACC"  
PN J07145197-A.  
PD 06-JUN-1995.  
PF 25-NOV-1993; JP-295393.  
PR 25-NOV-1993; JP-295393.  
PA (EISA ) EISAI CO LTD.  
DR WPI: 95-237197/31.  
DR N-PSDB: 091769.  
PT ETS transcription factor activated by ras - may be used in the study  
PT of cancer cell proliferation and the proliferation of the polyoma  
PT virus  
PS Claim 1; Page 7-9; 9pp; Japanese.  
CC The amino acid sequence of the novel ETS transcription factor family  
CC member - PEA3-beta. The gene was isolated from a HepG2 cell line cDNA

CC library. The probe for the screening was prepared by reverse  
 CC transcription on HepG2 mRNA followed by PCR using primers Q91770-1,  
 CC to produce a probe of 170-200 bp. The screening isolated the full  
 CC length sequence of the transcription factor. The gene was inserted into  
 CC the expression vectors pBluescript KS and pCDV1 for expression of the  
 CC protein in E.coli and COS7 cells, respectively. The ETS transcription  
 CC factor has specificity for and is activated by ras. It is useful as a  
 CC reagent in studies for the elucidation of the mechanism of cancer cell  
 CC multiplication or polyoma virus transformation of cells.  
 SQ Sequence 520 AA;

Query Match 4.2%; Score 14; DB 1; Length 520;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANYDKLSRS 308  
 DB 412 KNRPMANYDKLSRS 425

RESULT 3  
 W00167  
 ID W00167 standard; Protein: 462 AA.  
 AC W00167;  
 DT 25-APR-1997 (first entry)  
 DE E1AF matrix metalloproteinase regulator.  
 KW E1AF matrix metalloproteinase; regulator; infiltration; cancer;  
 KW metastasis; cell; control; antisense; decoy; DNA binding region;  
 KW target DNA; ribosome; induction; diagnosis; detection; treatment;  
 KW mammary cancer; fibrosarcoma; osteosarcoma; lung cancer.  
 OS Homo sapiens.  
 FH Key  
 FT domain  
 FT 315..399  
 FT Location/Qualifiers  
 FT domain  
 FT 126..222  
 FT /note="DNA binding domain"  
 FT region  
 FT 126..222  
 FT /note="glutamine rich region"  
 PD W09624379-A1.  
 PD 15-AUG-1996.  
 PR 09-JAN-1996; J00016.  
 PR 08-FEB-1995; JP-020173.  
 PA (TAKI) TAKARA SHUZO CO LTD.  
 PI Fujinaga K, Higashino F, Yoshida K.  
 PI WPI; 96-384227/38.  
 DR N-PSDB; T37087.  
 PT Control of cancer cell infiltration by E1AF gene expression  
 PT regulation - also diagnosis of cancer by detection of E1AF gene  
 PT expression products  
 PS Example 5; Pages 38-42; 65pp; Japanese.  
 CC The present sequence is the E1AF protein, which is a matrix  
 CC metalloproteinase regulator. The infiltration and metastasis of  
 CC cancer cells can be controlled by regulating the expression and  
 CC expression products of the E1AF gene. This may be accomplished by  
 CC inducing antisense DNA or RNA for the E1AF gene, a decoy gene  
 CC expressing the DNA binding region of the E1AF protein, the target  
 CC DNA for the DNA binding region of the E1AF protein or ribosomes  
 CC corresponding to the E1AF gene mRNA. Cancer can be diagnosed by  
 CC detecting E1AF gene expression products, e.g. E1AF protein or mRNA.  
 CC These methods may be used in the treatment and diagnosis of cancer,  
 CC e.g. mammary cancer, fibrosarcoma, osteosarcoma, lung cancer, etc.  
 SQ Sequence 462 AA;

Query Match 4.2%; Score 14; DB 1; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 363 KNRPMANYDKLSRS 308  
 DB 363 KNRPMANYDKLSRS 376

RESULT 4

W49010  
 ID W49010 standard; Protein: 555 AA.  
 AC W49010;  
 DT 20-OCT-1998 (first entry)  
 DE Polyomavirus PEA3 protein.  
 KW Polyomavirus enhancer activator; PEA3; tumour; suppressor; inhibitor;  
 KW transformation; HER-2; neu promoter; metastasis; cancer.  
 OS Polyomavirus.  
 PD W09830585-A2.  
 PD 16-JUL-1998.  
 PR 12-JAN-1998; U00880.  
 PR 10-JAN-1997; US-780835.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 PI Hung M, Xing X;  
 PI WPI; 98-399061/34.  
 DR N-PSDB; V32688.  
 PT Method for repressing transformation of cells - by contacting cell  
 PT with polyoma-virus enhancer activator 3, useful for, e.g. treating  
 PT or preventing cancer, tumorigenesis and metastasis  
 PS Disclosure; Page 71-72; 83pp; English.  
 CC This sequence represents a polyomavirus enhancer activator, PEA3. This  
 CC sequence is used in a method for repressing transformation in a cell  
 CC which involves contacting the cell with PEA3 to inhibit a transformed  
 CC phenotype. This sequence can also be used in a method to suppress the  
 CC growth of a tumour in a mammal comprising introducing to the mammal a  
 CC PEA3-encoding nucleic acid where the expression of PEA3 in the mammal  
 CC results in a decrease in the growth rate of the tumour. PEA3 can regulate  
 CC the HER-2/neu promoter by transcriptional repression and acts as a tumour  
 CC repressor. The PEA3 can be used for reducing a transforming,  
 CC tumorigenic or metastatic potential of a cell. It can be used for the  
 CC prevention and treatment of such transformation-driven events as cancer,  
 CC tumorigenesis and metastasis.  
 SQ Sequence 555 AA;

Query Match 4.2%; Score 14; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANYDKLSRS 308  
 DB 456 KNRPMANYDKLSRS 469

RESULT 5  
 R44556  
 ID R44556 standard; Protein: 452 AA.  
 AC R44556;  
 DT 26-MAY-1994 (first entry)  
 DE Human HDM-FLI-1 gene product.  
 KW Chromosomal translocation; chimeric; chimeric; Ewing sarcoma;  
 KW Ews gene; malignant melanoma; hum-fl1-1; clone BM025;  
 KW primitive peripheral neuroectodermal tumour; human chromosome 11;  
 KW human chromosome 22; ss.  
 OS Homo sapiens.  
 PN W09323549-A.  
 PN 25-NOV-1993.  
 PR 19-MAY-1993; F00494.  
 PR 20-MAY-1992; FR-006123.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 PI Aurias A, Delattre O, Desmaziere C, Melot T, Peter M;  
 PI Plougastel B, Thomas G, Zucman J;  
 DR N-PSDB; Q50644.  
 PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene  
 PT sequence involved in chromosomal translocation, also derived  
 PT mRNA, probes, fusion proteins etc., for diagnosis and treatment  
 PT of Ewing sarcoma and melanoma  
 PS Disclosure; Fig 7; 123pp; French.  
 CC The probe 11R1 was used to screen a human marrow cDNA library  
 CC (Clontech cat. # HL1058). The clone BM025 was identified and  
 CC sequenced. It represents the entire coding region together with  
 CC 5'- and 3'-UTRs of the Hum-Fl1-1 gene.

SO Sequence 452 AA:

Query Match 2.48: Score 8; DB 1; Length 452;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNYDKLSR 307  
Db 330 MNYDKLSR 337

RESULT 6

W07700 standard: Protein; 548 AA.

AC W07700: 06-APR-1997 (first entry)

DE Human ETS2 repressor factor (ERF).

KM ETS2 repressor factor; ERF; transcriptional repressor;

KM tumour suppressor; tumour; cancer; oncoprotein; therapy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain

FT /label= "DNA-binding\_domain

FT /note= "ets-like DNA binding domain"

FT domain 472..530

FT /label= "Active\_repressor\_domain

FT /note= "(Claim 20)"

FT W09639517-A1.

PD 12-DEC-1996.

PF 04-JUN-1996: U10177.

PR 05-JUN-1995: US-469412.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;

PI Sgouras D N;

DR WPI: 97-043139/04.

DR N-PSDB: T47198.

PT New DNA encoding ETS2 repressor factor - useful for reducing

PT tumourigenicity esp. oncogene associated tumour cells

PS Claim 1; Page 39-61; 101pp; English.

CC Novel human ETS2 repressor factor (ERF) (W07700) is the first member

CC of the ETS family to be identified as a transcriptional repressor in

CC mammalian cells. Its amino acid sequence was deduced from a cDNA

CC clone (T47198) derived from K562 cells. ERF and alternatively

CC spliced ERF (see also W07701) show no homology to other known

CC proteins. The ERF repressor domain in combination with a

CC heterologous transcription factor having a binding domain can

CC be used as novel transcriptional repressors to reduce

CC tumourigenicity associated with inappropriate expression of the

CC GAL4, NFkappaB (HIV), MYC (Burkitt lymphoma), Flt-1 (Ewing's

CC sarcoma) and Ets1 transcription factors.

SO Sequence 548 AA:

Query Match 2.48: Score 8; DB 1; Length 548;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNYDKLSR 307  
Db 76 MNYDKLSR 83

RESULT 7

W07702 standard: Protein; 543 AA.

AC W07702:

DT 06-APR-1997 (first entry)

DE Mouse ETS2 repressor factor (ERF).

KM ETS2 repressor factor; ERF; transcriptional repressor;

KM tumour suppressor; tumour; cancer; oncoprotein; therapy.

OS Mus sp.

FT Key Location/Qualifiers

FT domain

FT /label= "DNA-binding\_domain

FT /note= "ets-like DNA binding domain"

FT domain 466..525

FT /label= "Active\_repressor\_domain

FT W09639517-A1.

PD 12-DEC-1996.

PF 04-JUN-1996: U10177.

PR 05-JUN-1995: US-469412.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;

PI Sgouras D N;

DR WPI: 97-043139/04.

DR N-PSDB: T47200.

PT New DNA encoding ETS2 repressor factor - useful for reducing

PT tumourigenicity, esp. oncogene associated tumour cells

PS Disclosure; Page 70-72; 101pp; English.

CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS

CC family and acts as a transcriptional repressor in mammalian cells.

CC Its amino acid sequence was deduced from the murine ERF gene

CC (T47198). Human ERF (see also W07700) has also been identified.

CC ERF has tumour suppressor activity. Chimeric molecules comprising

CC the ERF repressor domain in combination with a heterologous

CC transcription factor having a binding domain can be used to reduce

CC tumourigenicity associated with inappropriate expression of

SO Sequence 543 AA:

Query Match 2.48: Score 8; DB 1; Length 543;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MNYDKLSR 307  
Db 68 MNYDKLSR 75

RESULT 8

Y01521 standard: Protein; 478 AA.

AC Y01521:

DT 14-JUN-1999 (first entry)

DE Chicken c-erg protein.

KM Chicken; C-11 protein; cell calcification inhibiting activity;

KM cell calcification inhibiting agent; c-erg protein; arthritis deformans;

KM ossification; spinal column ligament.

OS Gallus sp.

PN J1075871-A.

PD 23-MAR-1999.

PF 29-MAY-1998: 166076.

PR 20-JUN-1997: US-050297.

PR 18-JUN-1997: US-878177.

PA (CHUS ) CHUGAI PHARM CO LTD.

PA (UYPE-) UNIV PENNSYLVANIA.

DR WPI: 99-257708/22.

DR N-PSDB: X26552.

PT An active protein for inhibiting cell calcification - useful for

PT measuring the calcification of a cell, for diagnosing arthritis

PT deformans or ossification of spinal column ligament

PS Claim 5; Page 9-10; 15pp; Japanese.

CC The present sequence represents chicken c-erg protein. The specification

CC also describes a chicken C-11 protein (Y01520) which has cell

CC calcification inhibiting activity and a cell calcification inhibiting

CC agent containing c-erg protein. The proteins are used for measuring the

CC calcification of a cell, for diagnosing arthritis deformans or

CC ossification of spinal column ligament.

SO Sequence 478 AA:

Query Match 2.48: Score 8; DB 1; Length 478;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNVDKLSR 307  
DB 359 MNVDKLSR 366

## RESULT 9

ID Y01520  
AC Y01520: Y01520 standard: Protein: 451 AA.  
DT 23-JUN-1999 (first entry)  
DE Chicken C-11 protein.  
KW Chicken: C-11 protein; cell calcification inhibiting activity;  
cell calcification inhibiting agent; c-ery protein; arthritis deformans;  
OS ossification; spinal column ligament.  
PN Gallus sp.  
PD 21075871-A.  
PE 23-MAR-1999.  
PR 29-MAY-1998; 166076.  
PS 20-JUN-1997; US-050297.  
PR 18-JUN-1997; US-878177.  
PA (CHUS ) CHUGAI PHARM CO LTD.  
PI (UYPE-) UNIV PENNSYLVANIA.  
DR WPI: 99-257708/22.  
N-PSDB: X25551.  
PT An active protein for inhibiting cell calcification - useful for  
measuring the calcification of a cell, for diagnosing arthritis  
PT deformans or ossification of spinal column ligament  
PS Claim 1; Page 8; 15pp; Japanese.  
CC The present sequence represents a chicken C-11 protein which has cell  
calcification inhibiting activity. The specification also describes  
CC a cell calcification inhibiting agent containing c-ery protein (Y01521).  
CC The proteins are used for measuring the calcification of a cell, for  
diagnosing arthritis deformans or ossification of spinal column ligament.  
SQ Sequence 451 AA:

Query Match 2.4%; Score 8; DB 1; Length 451;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 300 MNVDKLSR 307  
DB 332 MNVDKLSR 339

## RESULT 10

ID P81328  
AC P81328: P81328 standard: Protein: 295 AA.  
DT 22-OCT-1990 (first entry)  
DE Immunoreactive human B-lymphotropic viral protein  
KW Immunoreactive; human B-lymphotropic virus.  
PN W068080814-A.  
PD 15-DEC-1988.  
PE 27-MAY-1988; U01807.  
PR 01-JUN-1987; US-056963.  
PA (BAYU) Baylor Univ College: (USSH) US Dept of Health and Human Services.  
PI Chang NT, Chang TW, Fung MS-C, Fung M-C, Gallo RC, Wong-Staal F;  
DR WPI: 88-368628/51.  
N-PSDB: N81720.  
PT New immunoreactive protein of human B lymphotropic virus - and encoding  
PT DNA sequences, useful as immunogens and for detecting specific Abs in  
PT blood  
PS Disclosure: P: English.  
CC This is used to detect antibodies against HBV in biological fluids (esp.  
CC for screening human serum or plasma).  
SQ Sequence 295 AA:

Query Match 2.1%; Score 7; DB 1; Length 295;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 VLKDIET 136  
DB 96 VLKDIET 102

## RESULT 11

ID R13016  
AC R13016: R13016 standard: Protein: 153 AA.  
DT 26-SEP-1991 (first entry)  
DE Deacetylcephalosporin C acetyltransferase N-terminal.  
KW DAC: deacetylcephalosporin C synthetase; DACCS;  
KW deacetylcephalosporin C synthetase; DACS; cefg gene.  
OS Acetemonium chrysogenum ATCC 14553.  
PN EP-437378-A.  
PD 17-JUL-1991.  
PE 11-JAN-1991; 300225.  
PR 12-JAN-1990; GB-000699.  
PR 20-APR-1990; GB-008876.  
PA (GLAX ) GLAXO GROUP LTD.  
PI Maistman NJ, Ramsden M;  
DR WPI: 91-209975/29.  
N-PSDB: Q12599.  
PT Recombinant DNA encoding deacetylcephalosporin - for high yield  
PT prodn. of cephalosporin C in transformed hosts, with increased  
PT stability and activity of enzyme  
PS Claim 3; Page 18; 22pp; English.  
CC The cefg gene encoding the DAC acetyltransferase enzyme is used in  
CC a recombinant DNA construct, excluding a gene encoding the native  
CC DACCS/DACS. The construct enables efficient introduction of  
CC multiple and/or modified copies of a DAC acetyltransferase-encoding  
CC DNA sequence in hosts and hence the potential accumulation of  
higher intracellular levels of cephalosporin C.  
SQ Sequence 153 AA:

Query Match 2.1%; Score 7; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 284 SAQVART 290  
DB 4 SAQVART 10

## RESULT 12

ID R42293  
AC R42293: R42293 standard: Protein: 444 AA.  
DT 10-MAY-1994 (first entry)  
DE Cephalosporium acremonium DAC-ATF.  
KW acetyl-CoA:deacetylcephalosporin C acetyltransferase; cefg gene;  
KW Acetemonium chrysogenum; antibiotic; biosynthesis; cefEF, ss.  
OS Cephalosporium acremonium (strain C10).  
PN EP-566897-A.  
PD 27-OCT-1993.  
PE 26-MAR-1993; 105016.  
PR 07-APR-1992; EP-105986.  
PA (FARH ) HOECHST AG.  
PI Fernandez PFU, Gutierrez M, Martin MJF, Velasco AJ;  
PI Fernandez Perrino FJ, Gutierrez Martin S, Martin Martin JF;  
PI Velasco Alvarez J;  
DR WPI: 93-337989/43.  
N-PSDB: O50118.  
PT Cefg. gene encoding DAC-ATF - used to enhance cephalosporin C  
PT prodn.  
PS Claim 2; Page 6; 11pp; English.  
CC The cefg gene of C. acremonium encodes a protein of 444 amino acids  
CC having mol.wt. 49269 and having acetyl-CoA:deacetylcephalosporin C  
CC acetyltransferase activity. The isolated cefg gene complements  
CC deacetylcephalosporin acetyltransferase deficiency and restores  
CC cephalosporin biosynthesis.

SQ Sequence 444 AA:

Query Match 2.1%; Score 7; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 284 SAOVARL 290  
 |||||  
 DB 4 SAOVARL 10

RESULT 13

ID R67430 standard; Protein: 346 AA.

AC R67430:  
 DT 30-AUG-1995 (first entry)  
 DE Thermostable aminopeptidase.  
 KW Aminopeptidase; thermostable; Pyrococcus furiosus; expression;  
 KM recombinant production  
 OS Pyrococcus furiosus DMS3638.  
 PN J06319566-A.  
 PD 22-NOV-1994.  
 PE 18-MAY-1993: 138876.  
 PR 18-MAY-1993: JP-138876.  
 PA (TAKI) TAKARA SHUZO CO LTD.  
 DR WPI: 95-040319/06.  
 DR N-PSDB: Q75345.  
 PT Highly thermostable aminopeptidase gene - allows mass production  
 PS Claim 2; Page 7-8: 10pp: Japanese.  
 CC Mass production of the aminopeptidase may be effected by  
 CC transforming a microbial host with a recombinant plasmid comprising  
 CC the aminopeptidase gene. The aminopeptidase is then expressed and  
 CC retrieved from the culture supernatant.  
 SO Sequence 346 AA;

Query Match 2.1%; Score 7; DB 1; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GASSREE 85  
 |||||  
 DB 139 GASSREE 145

RESULT 14

ID W31186 standard; Protein: 905 AA.

AC W31186:  
 DT 11-MAR-1998 (first entry)  
 DE Human p160 polypeptide 160.2.  
 KW p160; p62; cytoplasmic; T cell; B cell; development; activation;  
 KW modulation; cellular response; cell proliferation; autoimmune disease;  
 KM p56-lck.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Domain 3..138  
 FT Region 510..638  
 FT /note="proline/lysine rich region"  
 FT Region 654..870  
 FT /note="glutamic acid rich region"  
 PN W09122255-A1.  
 PD 26-JUN-1997.  
 PE 11-DEC-1996: U19944.  
 PR 19-DEC-1995: US-574959.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 PI Young I, Shin J, Strominger JL, Vladimirov RK.  
 DR WPI: 97-341351/31.  
 DR N-PSDB: T89346.  
 PT cDNA encoding p62 and p160 and corresponding proteins - used in the

PT treatment of autoimmune disease and for T and B cell proliferation,  
 PT e.g. for treatment of tumors

PS Claim 84; Fig 11; 175pp: English.  
 CC This sequence represents a novel p160 polypeptide (160.2) which is  
 CC capable of activating transcription of a variety of genes upon activation  
 CC of p62 and is capable of binding to the p62/p56lck complex to modulate  
 CC lck function in a manner similar to p62. The genes transcribed in  
 CC response to p160 activation likely include those of which are involved in  
 CC T or B cell development/differentiation, T or B cell activation or  
 CC production of T or B cell specific factors e.g. lymphokines or  
 CC antibodies. This p160 polypeptide is also a substrate for  
 CC serine/threonine kinase activity. p160 polypeptides can modulate  
 CC degradation of cellular proteins e.g. cell cycle regulatory proteins  
 CC stimulating expression of cell cycle dependent kinase inhibitors and  
 CC arresting cell cycle progression at specific boundaries to thereby  
 CC modulate cell proliferation. As p160 boosts B cell response it may be  
 CC used to treat disorders where this is beneficial, e.g. infections by  
 CC pathogenic microorganisms. p160 can be used to expand T cell populations  
 CC for treating infectious diseases or cancer and p160 inhibitors could  
 CC reduce B or T cell responses and may be used to treat a variety of  
 CC autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple  
 CC sclerosis allergic reactions and Crohn's disease.  
 SO Sequence 905 AA;

Query Match 2.1%; Score 7; DB 1; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 16+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PSHLLP 19  
 |||||  
 DB 361 PSHLLP 367

RESULT 15

ID W36503 standard; Protein: 543 AA.

AC W36503:  
 DT 22-APR-1998 (first entry)  
 DE Human hyaluronate synthetase.  
 KW Hyaluronate synthetase; human; hyaluronic acid; drug preparation;  
 KW cosmetic preparation; gene therapy; carcinogenesis.  
 OS Homo sapiens.  
 PN W09738113-A1.  
 PD 16-OCT-1997: J01111.  
 PF 31-MAR-1997: J01111.  
 PR 30-APR-1996: JP-109663.  
 PR 05-APR-1996: JP-084326.  
 PA (SEKK) SEIKAGAKU CORP.  
 PI Itano N, Kimata K.  
 DR WPI: 97-512726/47.  
 DR N-PSDB: T96713.  
 PT DNA encoding human hyaluronate synthetase - for industrial scale  
 PT production of hyaluronic acid used in generating anti-carcinogenic  
 PT drugs or for cosmetics  
 PS Claim 2; Page 23-27: 35pp: Japanese.  
 CC This sequence represents a human hyaluronate synthetase, and is encoded  
 CC by the coding sequence of the invention. This enzyme is useful for  
 CC industrial scale production of hyaluronic acid for use in the preparation  
 CC of drugs and cosmetics. The drugs can also be used in compositions for  
 CC the treatment of disorders involving the lowering of hyaluronic acid  
 CC production. The peptides may be used for the preparation of antibodies  
 CC recognising hyaluronate synthetase, e.g. for diagnostic purposes.  
 CC Antisense DNA or RNA corresponding to the DNA can be used in gene therapy  
 CC treatment of carcinogenesis.  
 SO Sequence 543 AA;

Query Match 2.1%; Score 7; DB 1; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 16+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 AAGAVG 37

|||||  
Db 138 AAAGAVG 144

Search completed: November 20, 1999, 15:35:23  
Job time: 165 sec

GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 1999, 15:32:38 : Search time 13.1 Seconds

(without alignments)  
605.713 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 335  
Sequence: 1 MGSASPGLSVSPSHLLPP.....GIIRKPDISQRLVYGFVHP1 335

Scoring table: OLIGO

Searched: 188963 seqs, 23686106 residues

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	4.2	155	1	R45451	Adenovirus E1A-F P
2	14	4.2	520	1	R78185	Protein sequence o
3	14	4.2	462	1	W00167	E1A matrix metal
4	14	4.2	555	1	W49010	Polyomavirus PEA3
5	8	2.4	452	1	R44556	Human HUN-FLI-1 ge
6	8	2.4	548	1	W07700	Human ETS2 repress
7	8	2.4	543	1	W07702	Mouse ETS2 repress
8	8	2.4	478	1	Y01521	Chicken C-11 prote
9	8	2.4	451	1	Y01520	Immunoreactive hum
10	7	2.1	295	1	P81328	Cephalosporium acr
11	7	2.1	153	1	R13016	Thermotable amino
12	7	2.1	444	1	R42293	Human p160 polypep
13	7	2.1	346	1	R67430	Human hyaluronate
14	7	2.1	905	1	W31186	Human hyaluronan s
15	7	2.1	543	1	W35503	Human secreted pro
16	7	2.1	578	1	W26765	Human lymphoid-spe
17	7	2.1	521	1	W47237	Human hyaluronate
18	7	2.1	581	1	W47238	Human lymphoid-spe
19	7	2.1	339	1	W75169	Human secreted pro
20	7	2.1	89	1	W97655	Urinary tract BL21
21	7	2.1	45	1	W97657	Human 5' EST secre
22	7	2.1	30	1	Y12590	Partial sequence o
23	6	1.8	14	1	P31133	Recombinant activa
24	6	1.8	294	1	P91468	Sequence of canine
25	6	1.8	191	1	P92071	Partial nucleotide
26	6	1.8	254	1	P93673	Sheep PRP gene for
27	6	1.8	256	1	P93674	Sequence of canine
28	6	1.8	3647	1	R05041	Sequence of the Ja
29	6	1.8	1295	1	R05597	Sequence of canine
30	6	1.8	421	1	R05801	Sequence of the Ja
31	6	1.8	471	1	R05923	Sequence of canine
32	6	1.8	471	1	R05924	Sequence of canine
33	6	1.8	1664	1	P82979	Sequence of the Ja
34	6	1.8	165	1	R07360	Sequence of the Ja
35	6	1.8	1706	1	R08031	Sequence of the Ja
36	6	1.8	1706	1	R08205	Sequence of the Ja
37	6	1.8	196	1	P70441	Adeny cyclase fro
38	6	1.8	927	1	P70468	Heat resistant per
39	6	1.8	927	1	P70468	Sequence encoded b
40	6	1.8	5072	1	R11510	Epstein-Barr virus
41	6	1.8	1445	1	R12108	N-terminal deleted
42	6	1.8	1705	1	P94365	Sequence of part o
43	6	1.8	283	1	P81096	Sequence of rhlno

44 6 1.8 1522 1 P93357 Sequence of the ca  
45 6 1.8 528 1 W96151 Salmonella SptP/LC

## ALIGNMENTS

## RESULT 1

ID R45451 standard; Protein: 155 AA.

AC R45451;

DT 11-JUL-1994 (first entry)

DE Adenovirus E1A-F protein.

KW Adenovirus: cancer; ets oncogene; Hela cell; enhancer core sequence;

KW methylation.

OS Human adenovirus.

PN J05328975-A.

PD 14-DEC-1993.

PF 02-JUN-1992: 165453.

PR 02-JUN-1992: JP-165453.

PA (TAKI ) TAKARA SHUZO CO LTD.

DR WPI: 94-021923/03.

DR N-PSDB: 055149.

PT Novel E1A-F gene - for production of adenovirus E1A-F and cancer

PT research

PS Claim 1; Page 5; 7pp; Japanese.

CC A clone comprising the adenovirus E1A-F gene was isolated by

CC screening a Hela cell cDNA library. The cDNA insert from the clone

CC contains a 473bp open reading frame which codes for a protein

CC having sequence R45451.

CC Sequence 155 AA;

Query Match 4.2%; Score 14; DB 1; Length 155;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMAMNDKLSRS 308

Db 56 KNRPMAMNDKLSRS 69

## RESULT 2

ID R78185 standard; Protein: 520 AA.

AC R78185;

DT 09-FEB-1996 (first entry)

DE Protein sequence of PEA3-Delta -an ETS transcription factor.

KW Transcription factor; Probe: reverse transcription; PCR; primer;

KW expression vector; E.coli; COS cell; ras; cancer cell multiplication;

KW polyoma virus; transformation.

OS Homo sapiens.

FS Homo sapiens. Location/Qualifiers

FT Key

FT misc\_difference 84

FT /note= "encoded by CTC"

FT misc\_difference 126

FT /note= "encoded by AAC"

FT misc\_difference 500

FT /note= "encoded by ACC"

PN J07145197-A.

PD 06-JUN-1995.

PF 25-NOV-1993: 295393.

PR 25-NOV-1993: JP-295393.

PA (EISA ) EISAI CO LTD.

PA (HIRA ) HIRANO T.

DR WPI: 95-237197/31.

DR N-PSDB: 091769.

PT ETS transcription factor activated by ras - may be used in the study

PT of cancer cell proliferation and the proliferation of the polyoma

PT virus

PS Claim 1; Page 7-9; 9pp; Japanese.

CC The amino acid sequence of the novel ETS transcription factor family

CC member - PEA3-beta. The gene was isolated from a HepG2 cell line cDNA

CC library. The probe for the screening was prepared by reverse  
CC transcription on HepG2 mRNA followed by PCR using primers 091770-1.  
CC to produce a probe of 170-200 bp. The screening isolated the full  
CC length sequence of the transcription factor. The gene was inserted into  
CC the expression vectors pBluescript KS and pCDV1 for expression of the  
CC protein in E.coli and COS7 cells, respectively. The ETS transcription  
CC factor has specificity for and is activated by ras. It is useful as a  
CC reagent in studies for the elucidation of the mechanism of cancer cell  
CC multiplication or polyoma virus transformation of cells.  
CC Sequence 520 AA;

Query Match 4.2%; Score 14; DB 1; Length 520;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMAMNDKLSRS 308

Db 412 KNRPMAMNDKLSRS 425

## RESULT 3

ID W00167 standard; Protein: 462 AA.

AC W00167;

DT 25-APR-1997 (first entry)

DE E1AF matrix metalloproteinase regulator.

KW E1AF; matrix; metalloproteinase; regulator; Infiltration; cancer;

KW metastasis; cell; control; antisense; decoy; DNA binding region;

KW target DNA; ribosome; induction; diagnosis; detection; treatment;

KW mammary cancer; fibrosarcoma; osteosarcoma; lung cancer.

OS Homo sapiens.

FS Homo sapiens. Location/Qualifiers

FT domain 315..399

FT /note= "DNA binding domain"

FT region 126..222

FT /note= "glutamine rich region"

PN W09624379-A1.

PD 15-AUG-1996.

PF 09-JAN-1996: J00016.

PR 08-FEB-1995: JP-020173.

PA (TAKI ) TAKARA SHUZO CO LTD.

PI Fujinaga K, Higashino F, Yoshida K;

DR WPI: 96-384227/38.

DR N-PSDB: T37087.

PT Control of cancer cell infiltration by E1AF gene expression

PT regulation - also diagnosis of cancer by detection of E1AF gene

PS Example 5; Pages 38-42; 65pp; Japanese.

CC The present sequence is the E1AF protein, which is a matrix

CC metalloproteinase regulator. The infiltration and metastasis of

CC cancer cells can be controlled by regulating the expression and

CC inducing antisense DNA or RNA for the E1AF gene, a decoy gene

CC expressing the DNA binding region of the E1AF protein, the target

CC DNA for the DNA binding region of the E1AF protein or ribosomes

CC corresponding to the E1AF gene mRNA. Cancer can be diagnosed by

CC detecting E1AF gene expression products, e.g. E1AF protein or mRNA.

CC These methods may be used in the treatment and diagnosis of cancer.

CC e.g. mammary cancer, fibrosarcoma, osteosarcoma, lung cancer, etc.

SO Sequence 462 AA;

Query Match 4.2%; Score 14; DB 1; Length 462;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMAMNDKLSRS 308

Db 363 KNRPMAMNDKLSRS 376

## RESULT 4

W49010  
ID W49010 standard; Protein; 555 AA.  
AC W49010;  
DT 20-OCT-1998 (first entry)  
DE Polyomavirus PEA3 protein.  
KW Polyomavirus enhancer activator; PEA3; tumour; suppressor; inhibitor;  
KW transformation; HER-2; neu promoter; metastasis; cancer.  
OS Polyomavirus.  
PN WO98030586-A2.  
PD 15-JUL-1998.  
PF 12-JAN-1998; U00880.  
PR 10-JAN-1997; US-780835.  
PI (TEXA ) UNIV TEXAS SYSTEM.  
PI Hung M, Xing X;  
PI WPI: 98-399061/34.  
DR N-PSDB: V32688.  
PT Method for repressing transformation of cells - by contacting cell  
PT with polyoma-virus enhancer activator 3, useful for, e.g. treating  
PT or preventing cancer, tumorigenesis and metastasis  
PS Disclosure: Page 71-72; 83pp; English.  
CC This sequence represents a polyomavirus enhancer activator, PEA3. This  
CC sequence is used in a method for repressing transformation in a cell  
CC which involves contacting the cell with PEA3 to inhibit a transformed  
CC phenotype. This sequence can also be used in a method to suppress the  
CC growth of a tumour in a mammal comprising introducing to the mammal a  
CC PEA3-encoding nucleic acid where the expression of PEA3 in the mammal  
CC results in a decrease in the growth rate of the tumour. PEA3 can regulate  
CC the HER-2/neu promoter by transcriptional repression and acts as a tumour  
CC repressor. The PEA3 can be used for reducing a transforming,  
CC tumorigenic or metastatic potential of a cell. It can be used for the  
CC prevention and treatment of such transformation-driven events as cancer,  
CC tumorigenesis and metastasis.  
SQ Sequence 555 AA:

Query Match 4.2%; Score 14; DB 1; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMNRYDKLSRS 308  
|||||  
DB 456 KNRPMNRYDKLSRS 469

RESULT 5  
R44556  
ID R44556 standard; Protein; 452 AA.  
AC R44556;  
DT 26-MAY-1994 (first entry)  
DE Human HUM-FLI-1 gene product.  
KW Chromosomal translocation; chimeric; chimaeric; Ewing sarcoma;  
KW Ews gene; malignant melanoma; hum-fl-1; clone BM025;  
KW primitive peripheral neuroectodermal tumour; human chromosome 11;  
KW human chromosome 22; ss.  
OS Homo sapiens.  
PN WO9323549-A.  
PD 25-NOV-1993.  
PF 19-NOV-1993; F00494.  
PR 20-MAY-1992; FR-006123.  
PI (CNRS ) CNRS CENT NAT RECH SCI.  
PI Aurias A, Delattre O, Desmaziere C, Melot T, Peter M;  
PI Plougastel B, Thomas G, Zucman J;  
PI WPI: 93-386580/48.  
DR N-PSDB: O50644.  
PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene  
PT sequence involved in chromosomal translocation, also derived  
PT mRNA, probes, fusion proteins etc., for diagnosis and treatment  
PT of Ewing sarcoma and melanoma  
PS Disclosure: Fig 7; 123pp; French.  
CC The probe 11R1 was used to screen a human marrow cDNA library  
CC (Clontech cat. # HL1058). The clone BM025 was identified and  
CC sequenced. It represents the entire coding region together with  
CC 5'- and 3'-UTRs of the Hum-Fl-1 gene.

SQ Sequence 452 AA:

Query Match 2.4%; Score 8; DB 1; Length 452;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNVDKLSR 307  
|||||  
DB 330 MNVDKLSR 337

RESULT 6  
W07700  
ID W07700 standard; Protein; 548 AA.  
AC W07700;  
DT 06-APR-1997 (first entry)  
DE Human ETS2 repressor factor (ERF).  
KW ETS2 repressor factor; ERF; transcriptional repressor;  
KW tumour suppressor; tumour; cancer; oncoprotein; therapy.  
OS Homo sapiens.  
PI Key Location/Qualifiers  
PI domain 29..106  
PI FT /label=DNA-binding-domain  
PI FT /note="ets-like DNA binding domain"  
PI FT 472..530  
PI FT /label=Active-repressor-domain  
PI FT /note="(Claim 20)"  
PN WO9639517-A1.  
PD 12-DEC-1996.  
PF 04-JUN-1996; U01177.  
PR 05-JUN-1995; US-469412.  
PI (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Athanasiou NA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;  
PI Sgouras D N;  
PI WPI: 97-043139/04.  
DR N-PSDB: T47198.  
PT New DNA encoding ETS2 repressor factor - useful for reducing  
PT tumorigenicity, esp. oncogene associated tumour cells  
PS Claim 1; Page 56-61; 101pp; English.  
CC Novel human ETS2 repressor factor (ERF) (W07700) is the first member  
CC of the ETS family to be identified as a transcriptional repressor in  
CC mammalian cells. Its amino acid sequence was deduced from a cDNA  
CC clone (T47198) derived from K562 cells. ERF and alternatively  
CC spliced ERF (see also W07701) show no homology to other known  
CC proteins. The ERF repressor domain in combination with a  
CC heterologous transcription domain having a binding domain can  
CC be used as novel transcriptional repressors to reduce  
CC tumorigenicity associated with inappropriate expression of the  
CC GAL4, NFkappaB (NF- $\kappa$ B), MYC (Burkitt lymphoma), Fli-1 (Ewing's  
CC sarcoma) and ETS1 transcription factors.  
SQ Sequence 548 AA:

Query Match 2.4%; Score 8; DB 1; Length 548;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 MNVDKLSR 307  
|||||  
DB 76 MNVDKLSR 83

RESULT 7  
W07702  
ID W07702 standard; Protein; 543 AA.  
AC W07702;  
DT 06-APR-1997 (first entry)  
DE Mouse ETS2 repressor factor (ERF).  
KW ETS2 repressor factor; ERF; transcriptional repressor;  
KW tumour suppressor; tumour; cancer; oncoprotein; therapy.  
OS Mus sp.  
PI Key Location/Qualifiers



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FT domain 21..98
FT /label= DNA_binding_domain
FT /note="ets-like DNA binding domain"
FT domain 466..525
FT /label= Active_repressor_domain

PN WO9639517-A1.
PD 12-DEC-1996.
PE 04-JUN-1996: US-010177.
PR 05-JUN-1995: US-469412.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Athanasios MA, Beal GO, Blair DG, Fisher RJ, Mavrothalassitis GJ.
PI Sgouras D N.
DR MPI: 97-043139/04.
DR N-PSDB: T47200.
PT New DNA encoding ETS2 repressor factor - useful for reducing
PT tumourigenicity, esp. oncogene associated tumour cells
PS Disclosure: Page 70-72: 101pp: English.
CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS
CC family and acts as a transcriptional repressor in mammalian cells.
CC Its amino acid sequence was deduced from the murine ERF gene
CC (T47198). Human ERF (see also W07700) has also been identified.
CC ERF has tumour suppressor activity. Chimeric molecules comprising
CC the ERF repressor domain in combination with a heterologous
CC transcription factor having a binding domain can be used to reduce
CC tumourigenicity associated with inappropriate expression of
CC transcription factors.
SQ Sequence 543 AA:

Query Match 2.4%: Score 8; DB 1; Length 543;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MMYDKLSR 307
   |||||||
Db 68 MMYDKLSR 75

RESULT 8
Y01521 8
ID Y01521 standard; protein; 478 AA.
AC Y01521;
DT 14-JUN-1999 (first entry)
DE Chicken c-erg protein.
KW Chicken; C-11 protein; cell calcification inhibiting activity;
KW cell calcification inhibiting agent; c-erg protein; arthritis deformans;
KW ossification; spinal column ligament.
OS Gallus sp.
PN J1075871-A.
PD 23-MAR-1999.
PE 29-MAY-1998: 166076.
PR 20-JUN-1997: US-050297.
PR 18-JUN-1997: US-878177.
PA (CHUS ) CHUGAI PHARM CO LTD.
PA (TYPE-) UNIV PENNSYLVANIA.
DR MPI: 99-257708/22.
DR N-PSDB: X26552.
PT An active protein for inhibiting cell calcification - useful for
PT measuring the calcification of a cell, for diagnosing arthritis
PT deformans or ossification of spinal column ligament
PS Claim 5; Page 9-10: 15pp: Japanese.
CC The present sequence represents chicken c-erg protein. The specification
CC also describes a chicken C-11 protein (Y01520) which has cell
CC calcification inhibiting activity and a cell calcification inhibiting
CC agent containing c-erg protein. The proteins are used for measuring the
CC calcification of a cell, for diagnosing arthritis deformans or
CC ossification of spinal column ligament.
SQ Sequence 478 AA:

Query Match 2.4%: Score 8; DB 1; Length 478;
Best Local Similarity 100.0%: Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 300 MMYDKLSR 307
   |||||||
Db 359 MMYDKLSR 366

RESULT 9
Y01520 9
ID Y01520 standard; protein; 451 AA.
AC Y01520;
DT 23-JUN-1999 (first entry)
DE Chicken C-11 protein.
KW Chicken; C-11 protein; cell calcification inhibiting activity;
KW cell calcification inhibiting agent; c-erg protein; arthritis deformans;
KW ossification; spinal column ligament.
OS Gallus sp.
PN J1075871-A.
PD 23-MAR-1999.
PE 29-MAY-1998: 166076.
PR 20-JUN-1997: US-050297.
PR 18-JUN-1997: US-878177.
PA (CHUS ) CHUGAI PHARM CO LTD.
PA (TYPE-) UNIV PENNSYLVANIA.
DR MPI: 99-257708/22.
DR N-PSDB: X26551.
PT An active protein for inhibiting cell calcification - useful for
PT measuring the calcification of a cell, for diagnosing arthritis
PT deformans or ossification of spinal column ligament
PS Claim 1; Page 8: 15pp: Japanese.
CC The present sequence represents a chicken C-11 protein which has cell
CC calcification inhibiting activity. The specification also describes
CC a cell calcification inhibiting agent containing c-erg protein (Y01521).
CC The proteins are used for measuring the calcification of a cell, for
CC diagnosing arthritis deformans or ossification of spinal column ligament.
SQ Sequence 451 AA:

Query Match 2.4%: Score 8; DB 1; Length 451;
Best Local Similarity 100.0%: Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 MMYDKLSR 307
   |||||||
Db 332 MMYDKLSR 339

RESULT 10
P81328 10
ID P81328 standard; protein; 295 AA.
AC P81328;
DT 22-OCT-1990 (first entry)
DE Immunoreactive human B-lymphotropic viral protein
KW Immunoreactive; human B-lymphotropic virus.
PN WO8809814-A.
PD 15-DEC-1988.
PE 27-MAY-1988: U01807.
PR 01-JUN-1987: US-056963.
PA (BAYU) Baylor Univ College; (USSH) US Dept of Health and Human Services.
PA Chang NT, Chang FW, Fung MS-C, Fung M-C, Gallo RC, Wong-Steal F.
PI MPI: 88-368628/51.
PI WPI: 88-368628/51.
DR N-PSDB: N81720.
PT New immunoreactive protein of human B lymphotropic virus - and encoding
PT DNA sequences, useful as immunogens and for detecting specific Abs in
PT blood
PS Disclosure: P: English.
CC This is used to detect antibodies against HBV in biological fluids (esp.
CC for screening human serum or plasma).
SQ Sequence 295 AA:

Query Match 2.1%: Score 7; DB 1; Length 295;
Best Local Similarity 100.0%: Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 130 VLKDIET 136  
 |||||  
 DB 96 VLKDIET 102

## RESULT 11

R13016  
 ID R13016 standard; Protein: 153 AA.  
 AC R13016:  
 DT 26-SEP-1991 (first entry)  
 DE Deacetylcephalosporin C acetyltransferase N-terminal.  
 KW DAC; deacetoxycephalosporin C synthetase; DAOCS;  
 OS deacetylcephalosporin C synthetase; DACS; cefg gene.  
 PN Acremonium chrysogenum ATCC 14553.  
 PD EP-437378-A.  
 PF 17-JUL-1991.  
 PR 11-JAN-1991: 300225.  
 PR 12-JAN-1990; GB-000699.  
 PR 20-APR-1990; GB-008876.  
 PA (GLAXO) GLAXO GROUP LTD.  
 PI Maishman NJ, Ramsden M;  
 DR WPI: 91-209975/29.  
 DR N-PSDB: 012599.  
 PT Recombinant DNA encoding de:acetyl:cephalosporin - for high yield  
 PT prodn. of cephalosporin C in transformed hosts, with increased  
 PT stability and activity of enzyme  
 PS Claim 3; Page 18; 22pp: English.  
 CC The cefg gene encoding the DAC acetyltransferase enzyme is used in  
 CC a recombinant DNA construct, excluding a gene encoding the native  
 CC DAOCS/ACS. The construct enables efficient introduction of  
 CC multiple and/or modified copies of a DAC acetyltransferase-encoding  
 CC DNA sequence in hosts and hence the potential accumulation of  
 CC higher intracellular levels of cephalosporin C.  
 SQ Sequence 153 AA:

Query Match  
 Best Local Similarity 2.1%; Score 7; DB 1; Length 153;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 284 SAQVART 290  
 |||||  
 DB 4 SAQVART 10

## RESULT 12

R42293  
 ID R42293 standard; Protein: 444 AA.  
 AC R42293:  
 DT 10-MAY-1994 (first entry)  
 DE Cephalosporium acremonium DAC-ATF.  
 KW acetyl-CoA:deacetylcephalosporin C acetyltransferase; cefg gene;  
 OS Acremonium chrysogenum; antibiotic; biosynthesis; cefg; ss.  
 PN Cephalosporium acremonium (strain C10).  
 PD EP-56897-A.  
 PF 27-OCT-1993.  
 PR 26-MAR-1993: 105016.  
 PR 07-APR-1992; EP-105986.  
 PA (PARH) HOECHST AG.  
 PI Fernandez PJ, Gutierrez M, Martin MJF, Velasco AJ;  
 PI Fernandez Perrino FJ, Gutierrez Martin S, Martin Martin JF;  
 DR Velasco Alvarez J;  
 DR WPI: 93-337989/43.  
 DR N-PSDB: 050118.  
 PT Cefg. gene encoding DAC-ATF - used to enhance cephalosporin C  
 PT prodn.  
 PS Claim 2; Page 6; 11pp: English.  
 CC The cefg gene of C. acremonium encodes a protein of 444 amino acids  
 CC having mol. wt. 49269 and having acetyl-CoA:deacetylcephalosporin C  
 CC acetyltransferase activity. The isolated cefg gene complements  
 CC deacetylcephalosporin acetyltransferase deficiency and restores  
 CC cephalosporin biosynthesis.

SQ Sequence 444 AA;

Query Match  
 Best Local Similarity 2.1%; Score 7; DB 1; Length 444;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 284 SAQVART 290  
 |||||  
 DB 4 SAQVART 10

## RESULT 13

R67430  
 ID R67430 standard; Protein: 346 AA.  
 AC R67430:  
 DT 30-AUG-1995 (first entry)  
 DE Thermostable aminopeptidase.  
 KW Aminopeptidase; Thermostable; Pyrococcus furiosus; expression;  
 OS recombinant production.  
 OS Pyrococcus furiosus DMS3638.  
 PN J06319566-A.  
 PD 22-NOV-1994.  
 PF 18-MAY-1993: 138876.  
 PR 18-MAY-1993; JP-138876.  
 PA (TAKI) TAKARA SHUZO CO LTD.  
 DR WPI: 95-040319/06.  
 DR N-PSDB: 075345.  
 PT Highly thermostable aminopeptidase gene - allows mass production  
 PT of aminopeptidase by culture of transformed organisms  
 PS Claim 2; Page 7-8; 10pp: Japanese.  
 CC Mass production of the aminopeptidase may be effected by  
 CC transforming a microbial host with a recombinant plasmid comprising  
 CC the aminopeptidase gene. The aminopeptidase is then expressed and  
 CC retrieved from the culture supernatant.  
 SQ Sequence 346 AA:

Query Match  
 Best Local Similarity 2.1%; Score 7; DB 1; Length 346;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 GASSREE 85  
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 DB 139 GASSREE 145

## RESULT 14

W31186  
 ID W31186 standard; Protein: 905 AA.  
 AC W31186:  
 DT 11-MAR-1998 (first entry)  
 DE Human p160 polypeptide 160.2.  
 KW p160; p62; cytoplasmic; T cell; B cell; development; activation;  
 KW modulation; cellular response; cell proliferation; autoimmune disease;  
 KW p56-lck.  
 OS Homo sapiens.  
 FH Key  
 FH Domain  
 FT Location/Qualifiers  
 FT 3..138  
 FT /label= leucine\_zipper  
 FT 510..638  
 FT /note= "proline/lysine rich region"  
 FT 654..870  
 FT /note= "glutamic acid rich region"  
 FT Region  
 FT W09722255-A1.  
 PN 26-JUN-1997.  
 PD 26-JUN-1997.  
 PF 11-DEC-1996: U19944.  
 PR 19-DEC-1995: US-574959.  
 PA (DAND) DANA FARBER CANCER INST INC.  
 PI Jung I, Shin J, Strominger JL, Vadamudi RK;  
 DR WPI: 97-34151/31.  
 DR N-PSDB: T89346.  
 PT cDNA encoding p62 and p160 and corresponding proteins - used in the

PT treatment of autoimmune disease and for T and B cell proliferation.  
 PT e.g. for treatment of tumours  
 PS Claim 84; Fig 11; 175pp; English.  
 CC This sequence represents a novel p160 polypeptide (160.2) which is  
 CC capable of activating transcription of a variety of genes upon activation  
 CC of p52 and is capable of binding to the p52/p56lck complex to modulate  
 CC lck function in a manner similar to p62. The genes transcribed in  
 CC response to p160 activation likely include those of which are involved in  
 CC T or B cell development/differentiation, T or B cell activation or  
 CC production of T or B cell specific factors e.g. lymphokines or  
 CC antibodies. This p160 polypeptide is also a substrate for  
 CC serine/threonine kinase activity. p160 polypeptides can modulate  
 CC degradation of cellular proteins e.g. cell cycle regulatory proteins  
 CC stimulating expression of cell cycle dependent kinase inhibitors and  
 CC arresting cell cycle progression at specific boundaries to thereby  
 CC modulate cell proliferation. As p160 boosts B cell response it may be  
 CC used to treat disorders where this is beneficial, e.g. infections by  
 CC pathogenic microorganisms. p160 can be used to expand T cell populations  
 CC for treating infectious diseases or cancer and p160 inhibitors could  
 CC reduce B or T cell responses and may be used to treat a variety of  
 CC autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple  
 CC sclerosis allergic reactions and Crohn's disease.  
 SQ Sequence 905 AA;

Query Match 2.18; Score 7; DB 1; Length 905;  
 Best Local Similarity 100.08; Pred. No. 1.e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PSHLLP 19  
 |||||  
 Db 361 PSHLLP 367

RESULT 15  
 W36503  
 ID W36503 standard; Protein: 543 AA.  
 AC W36503;  
 DT 22-APR-1998 (first entry)  
 DE Human hyaluronate synthetase.  
 KW Hyaluronate synthetase; human; hyaluronic acid; drug preparation;  
 KM cosmetic preparation; gene therapy; carcinogenesis.  
 OS Homo sapiens.  
 PN W0973813-A1.  
 PD 16-OCT-1997.  
 PF 31-MAR-1997; J01111.  
 PR 30-APR-1996; JP-109663.  
 PR 05-APR-1996; JP-084326.  
 PA (SECK ) SEIKAGAKU CORP.  
 PI Itano N, Kimata K;  
 PI WPI: 97-512726/47.  
 DR N-PSDB: T96713.  
 DR DNA encoding human hyaluronate synthetase - for industrial scale  
 PT production of hyaluronic acid used in generating anti-carcinogenic  
 PT drugs or for cosmetics  
 PS Claim 2; Page 23-27; 35pp; Japanese.  
 CC This sequence represents a human hyaluronate synthetase, and is encoded  
 CC by the coding sequence of the invention. This enzyme is useful for  
 CC industrial scale production of hyaluronic acid for use in the preparation  
 CC of drugs and cosmetics. The drugs can also be used in compositions for  
 CC the treatment of disorders involving the lowering of hyaluronic acid  
 CC production. The peptides may be used for the preparation of antibodies  
 CC recognising hyaluronate synthetase, e.g. for diagnostic purposes.  
 CC Antisense DNA or RNA corresponding to the DNA can be used in gene therapy  
 CC treatment of carcinogenesis.  
 SQ Sequence 543 AA;

Db 138 AAAGAVG 144  
 |||||  
 Search completed: November 20, 1999, 15:35:23  
 Job time: 165 sec

Query Match 2.18; Score 7; DB 1; Length 543;  
 Best Local Similarity 100.08; Pred. No. 1.e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 AAAGAVG 37

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